

1 ATTCTCCCATTTCTCCCTCCCTCTCCCTTCTCCCTCTCCCTACTGGCTCCTCGTTTCTCTCC 60  
61 ATCTGCCTGACTCCTTGGGACCCGGTCCCCAGCTCGAGGATGGCGTCCTCTCTGCTTGAG 120  
M A S S L L E 7  
121 GAAGAAGCTCACTATGGCTCCAGTCCCCTGGCCATGCTGACTGCAGCCTGCAGCAAATTT 180  
8 E E A H Y G S S P L A M L T A A C S K F 27  
181 GGCGGCTCTAGCCCTCTGCGGGACTCAACAACCCTGGGGAAAGGAGGCACAAAGAAGCCA 240  
28 G G S S P L R D S T T L G K G G T K K P 47  
241 TACGCTGACCTTTTCAAGCCCCAAAACCATGGGGGACGCCTACCCAGCTCCCTTCTCAAGC 300  
48 Y A D L S A P K T M G D A Y P A P F S S 67  
301 ACCAATGGACTCCTCTCTCCTGCAGGCAGTCTCCGGCCCCAGCCTCTGGCTATGCAAAT 360  
68 T N G L L S P A G S P P A P A S G Y A N 87  
361 GACTACCCACCCTTCCCTCACTCATTTCCTGGGCCCACCGGTGCCCAAGACCCTGGGCTC 420  
88 D Y P P F P H S F P G P T F A Q D P G L 107  
421 CTAGTGCCTAAGGGGACAGCTCGTCTGACTGCCTGCTAGTGTCTACACTTCCCTGGAT 480  
108 L V P K G K S S S D C L P S V Y T S L D 127  
481 ATGACTCATCCCTATGGCTCGTGGTACAAGGCAGGCATCCACGCAGGCATCTCACCAGGT 540  
128 M T H P Y G S W Y K A G I K A G I S P G 147  
541 CCAGGCAACACACCTACTCCTTGGTGGGACATGCACCCTGGGGGCAACTGGCTAGGTGGT 600  
148 P G N T P T P W W D M H P G G N W L G G 167  
601 GGTCAGGGCCAGGGTGATGGGCTGCAAGGGACACTGTCCACAGGCCCTGCCAGCCTCCA 660  
168 G Q G Q G D G L Q G T L S T G P A Q P P 187  
661 CTGAACCCCCAGCTGCCTACTTACCCATCTGACTTTGCTCCCCTTAACCCAGCTCCCTAC 720  
188 L N P Q L P T Y P S D F A P L N P A P Y 207  
721 CCAGCGCCCCACCTCTTGCAACCAGGGCCCCAGCATGTCCTACCCCAAGATGTCTATAAG 780  
208 P A P H L L Q P G P Q H V L P Q D V Y K 227  
781 CCAAGGCGGTTGGCAATAGTGGGCAACTGGAGGGGAGTGGTGCAGCCAAACCCCTCGG 840  
228 P K A V G N S G Q L E G S G A A K P P R 247  
841 GGTGCTGGCACAGGGGGCAGCGGTGGATATGCGGGCAGTGGGGCAGGGCGTTCTACCTGC 900  
248 G A G T G G S G G Y A G S G A G R S T C 267  
901 GACTGCCCCAACTGTCAGGAGCTAGAGCGGCTCGGGGCAGCAGCGGCTGGGCTGAGGAAG 960  
268 D C P N C Q E L E R L G A A A A G L R K 287  
961 AAGCCCATTACAGCTGCCACATCCCTGGGTGCGGCAAGGTGTACGGCAAGGCTTCGCAT 1020  
288 K P I H S C H I P G C G K V Y G K A S H 307  
1021 CTGAAAGCCCCTTGCCTGGCAGACTGGCGAGAGGCCTTTTCGTCTGCAACTGGCTTTTC 1080  
308 L K A H L R W H T G E R P F V C N W L F 327  
1081 TGCGGCAAGAGGTTCACTCGCTCTGACGAGCTGGAGCGCCACGTGCGCACTCACACCCGG 1140  
328 C G K R F T R S D E L E R H V R T H T R 347  
1141 GAGAAGAAGTTCACTTGCCTGCTCTGTTCCAAGCGCTTTACCAGAAGCGACCACTTGAGC 1200  
348 E K K F T C L L C S K R F T R S D H L S 367  
1201 AAACATCAGCGCACCCACGGGGAGCCAGGCCCGGGACCGCCCCCAAGTGGCCCTAAGGAG 1260  
368 K H Q R T H G E P G P G P P P S G P K E 387

**FIG. 1A-1**

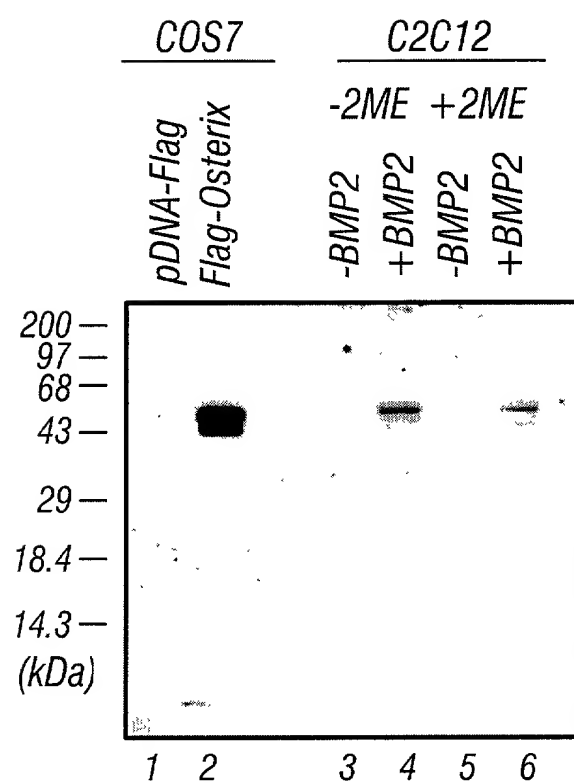
1261 CTGGGGGAGGGTCGCAGCGTCGGGGAAGAAGAAGCCAATCAGCCGCCCCGATCTTCCACT 1320  
 388 L G E G R S V G E E E A N Q P P R S S T 407  
 1321 TCGCCTGCACCCCCAGAAAAAGCCCACGGAGGCAGCCAGAGCAGAGCAACCTGCTAGAG 1380  
 408 S P A P P E K A H G G S P E Q S N L L E 427  
 1381 ATCTGAGCCGGGTAGAGGAAGGTCTCCAGCTCCAGGGTCCTCTTGCCAGGCTCTCTTGGC 1440  
 428 I \*  
 1441 GTGCTGGACCCATTGGTTGCCCTCGCTCTCTCCTATTGCATGCTATACTCTGGGGGCTC 1500  
 1501 TCTCTGTTCCCCTAGGCTATCTCCTTGCATGTCTCCTCAGTTCTTCTCTCTTTGTCAAGA 1560  
 1561 GTCTTAGCCAAACTCCTCTCAGGCCTTTGCCAGTGCCTAGTTCCTATGCTCCGACCTCCT 1620  
 1621 CAACTTTTTTCTTCTCTGCCCCTGTTCTTCACAGCTTCCATCTGGCCTCACATCATTTTTCT 1680  
 1681 CATTAACTCGTTGCCATCTAATCTTTCTGCTTCCCAATCCTATTTGCCGTTTTCCCGAAG 1740  
 1741 CTTCCAGGCTGTGCGCTCGATTCCCCCCCACCTTTTCGTCTTCCTGAGCTTTGTGTTTTCT 1800  
 1801 TTTTTTAAACAAACACGATGATGATGATGATGATGATAATTTATTGCCCCCTGGTGT 1860  
 1861 TCTTCATTAGGAACCAGAGTTAAGGAGATTGGTGTTAGTAACCTGGCCGGGAGCAGAGTG 1920  
 1921 CCAAGAAGGGGGAAGTCCAATGGGGATCTGATCCCAAAGATGGGGTGACCCCAGGGTCAG 1980  
 1981 GGAGGCTGCCCCAGCCTTGAGTACTTAACCCCTATGCGCCAGGAGTAAAGAATAGTAAT 2040  
 2041 AGTAATAATAATAATAATTCTATTTATCTAAGTTATGATGACGGGTGAGGTACAGTGAGC 2100  
 2101 TGGAGAGGGGAAAGGGATTCTCCCCGCCCCCAAGGAAATTCTAGTCAAATGCATCTCTGTA 2160  
 2161 TAGACAAATGATAGTGAGACCTTGCTCGTAGATTTCTATCCTCGAGGTCTCCGAGAGTT 2220  
 2221 TCTTTTTCAGTTGAGTTTTGGGTTGTTTCGGCCTCTTTTAGAGTTTCTGTGGGTGTCTCTC 2280  
 2281 TGTTAGGCAGTCACTAAGATCCCCAGCCCCAGCCAGAAAGCTGTGAAACTTCAAGTCCTA 2340  
 2341 TGGCGGGGAGGACTGGAATGTACCCAGTCCTCTCGACCCGACTGCAGATCAGGTTCCCTC 2400  
 2401 CCCTGATCCTCTTCTCATACCCTGTGACCTCACCAGGTTATCCCCTTGTCGTCATGGTTA 2460  
 2461 CAGAGAGCTTGCAGCTGCCATCTTAAACGTGCTCTTTGGGGGAGAGCCACCTAACAGGA 2520  
 2521 GGATTTTGGTTTGGAGGTGCCCCCTCTGAAAAAGTAGGTGGGCAAAGGCTTTCTCTGGGA 2580  
 2581 TCAAATTCAAATAAATCAAGTATTTATTGAATGCTTAATATGTGCAAGGCCTGGTGCCTA 2640  
 2641 GAAGCCACGAGAAAGAATTTATAACAGGACAGAAGTCCCTAAACTAAACATCCACAGGCC 2700  
 2701 CCCAATCTAGGAGGTTTCACTCCATTCCAGTGACTTTTAAAGCCGCTTTGTGCCTTTGAA 2760  
 2761 ATGCCTTTCTGAGATTTTTGGATCTTCCTGTTCTGTCCCCTGCTCCTTCTAGGCCTCAA 2820  
 2821 GATAAAGGGTAAAGCCATGGAGTCTGGGAAGAGCATAACGTGTTGACGGGATCGTCCCT 2880  
 2881 TTGTGGAATCTTTCTTTTTTTTTTAATTTAATAAATAAAAGTTCGATTTCAAAAAAAAAA 2900  
 2901 AAAAAAAAAAAAAAAAAAAAAA 2960

**FIG. 1A-2**

% IDENTITY

[illegible]

**FIG. 1B**



**FIG. 2**

MOUSE 1 MASSLLEEEAHYGSSPLAMLTAACSKFGGSSPLRDSTTLGKGGTKKPYA- 50  
 |||||  
 HUMAN 1 MASSLLEEEVHYGSSPLAMLTAACSKFGGSSPLRDSTTLGKAGTKKPYSV 50

MOUSE 51 --DLSAPKTMGDAYPAPFSSTNGLLSPAGSPAPASGYANDYPPFPHSFP 100  
 |||||  
 HUMAN 51 GSDLSASKTMGDAYPAPFTSTNGLLSPAGSPAPTSGYANDYPPFSHSFP 100

MOUSE 101 GPTGAQDPGLLVPKGHSDDCLPSVYTSMDTHPYGSWKAGIHAGISPG 150  
 |||||  
 HUMAN 101 GPTGTQDPGLLVPKGHSDDCLPSVYTSMDTHPYGSWKAGIHAGISPG 150

MOUSE 151 PGNTPTPWDMHPGGNWLGGGQGQDGLQGTLPSTGPAQPPLNPQLPTYP 200  
 |||||  
 HUMAN 151 PGNTPTPWDMHPGGNWLGGGQGQDGLQGTLPSTGPAQPPLNPQLPTYP 200

MOUSE 201 DFAPLNPAPYPAPHLLQPGPQHVL PQDVYKPKAVGNSGQLEGSGAAKPPR 250  
 |||||  
 HUMAN 201 DFAPLNPAPYPAPHLLQPGPQHVL PQDVYKPKAVGNSGQLEGSGGAKPPR 250

MOUSE 251 GAGTGGSGGYAGSGAGRSTCDPCNCQELERLGAAAAGLRKKPIHSCHIPG 300  
 || |||||  
 HUMAN 251 GASTGGSGGYGGSGAGRSSCDPCNCQELERLGAAAAGLRKKPIHSCHIPG 300

MOUSE 301 CGKVYKASHLKAHLRWHTGERPFVCNWLFCGKRFTSRDELERHVRTHTR 350  
 |||||  
 HUMAN 301 CGKVYKASHLKAHLRWHTGERPFVCNWLFCGKRFTSRDELERHVRTHTR 350

MOUSE 351 EKKFTCLLCSKRFTRSDHLSKHQRTHGEPGPGPPPSGPKELGEGRSVGEE 400  
 |||||  
 HUMAN 351 EKKFTCLLCSKRFTRSDHLSKHQRTHGEPGPGPPPSGPKELGEGRSTGEE 400

MOUSE 401 EANQPPRSSTSPAPPEKAHGGSPQSNLLEI 428  
 || |||||  
 HUMAN 401 EASQTPRPSASPATPEKAPGGSPEQSNLLEI 431

**FIG. 3**

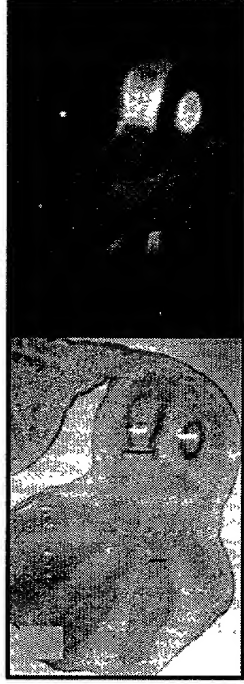


FIG. 3A

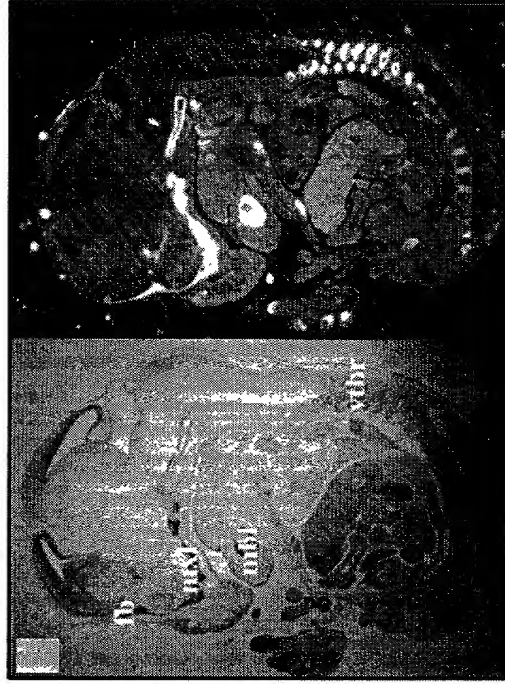


FIG. 3B



FIG. 3C

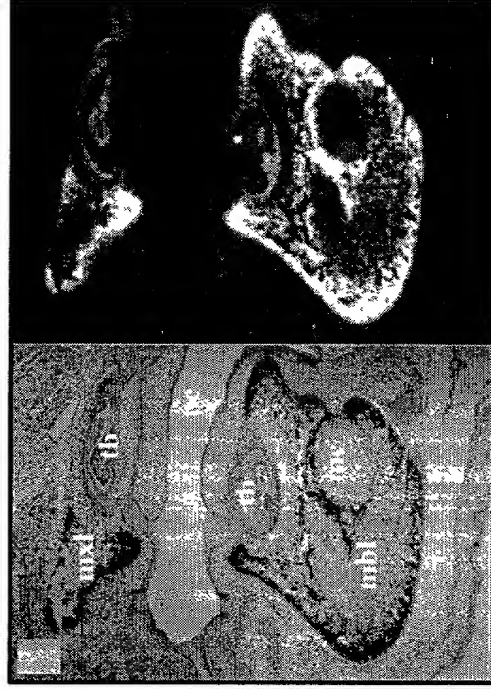


FIG. 3D

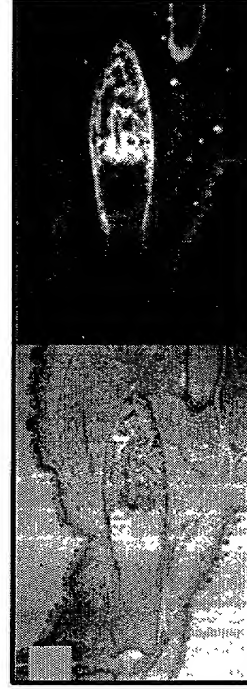


FIG. 3E

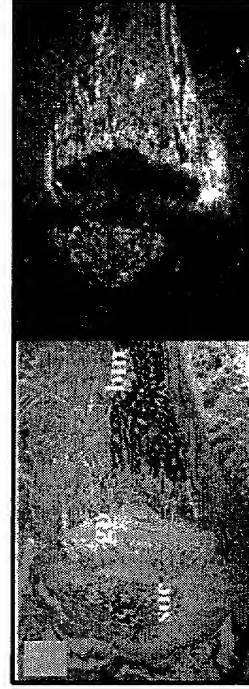
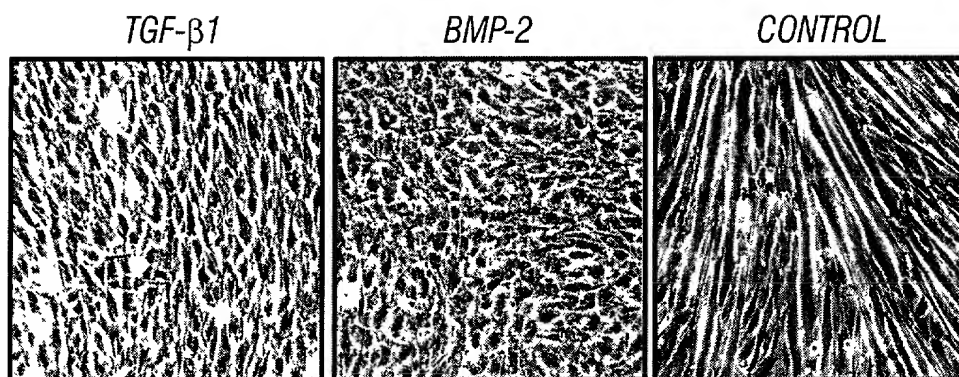
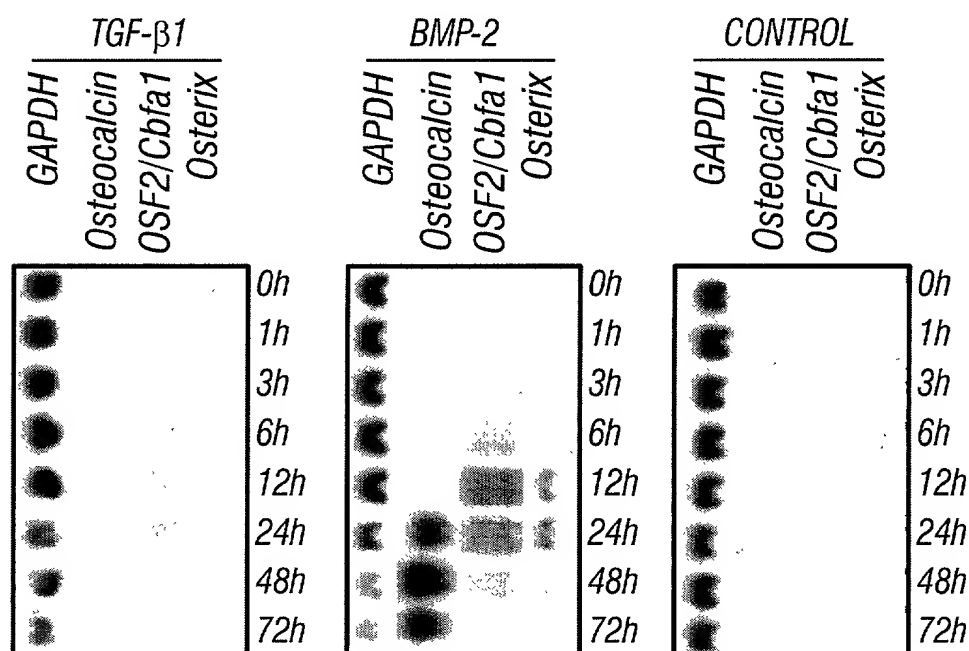


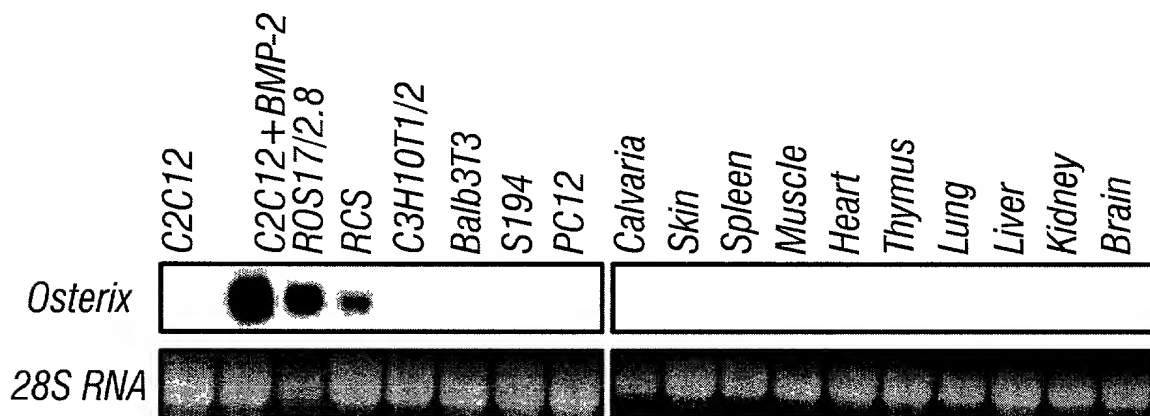
FIG. 3F



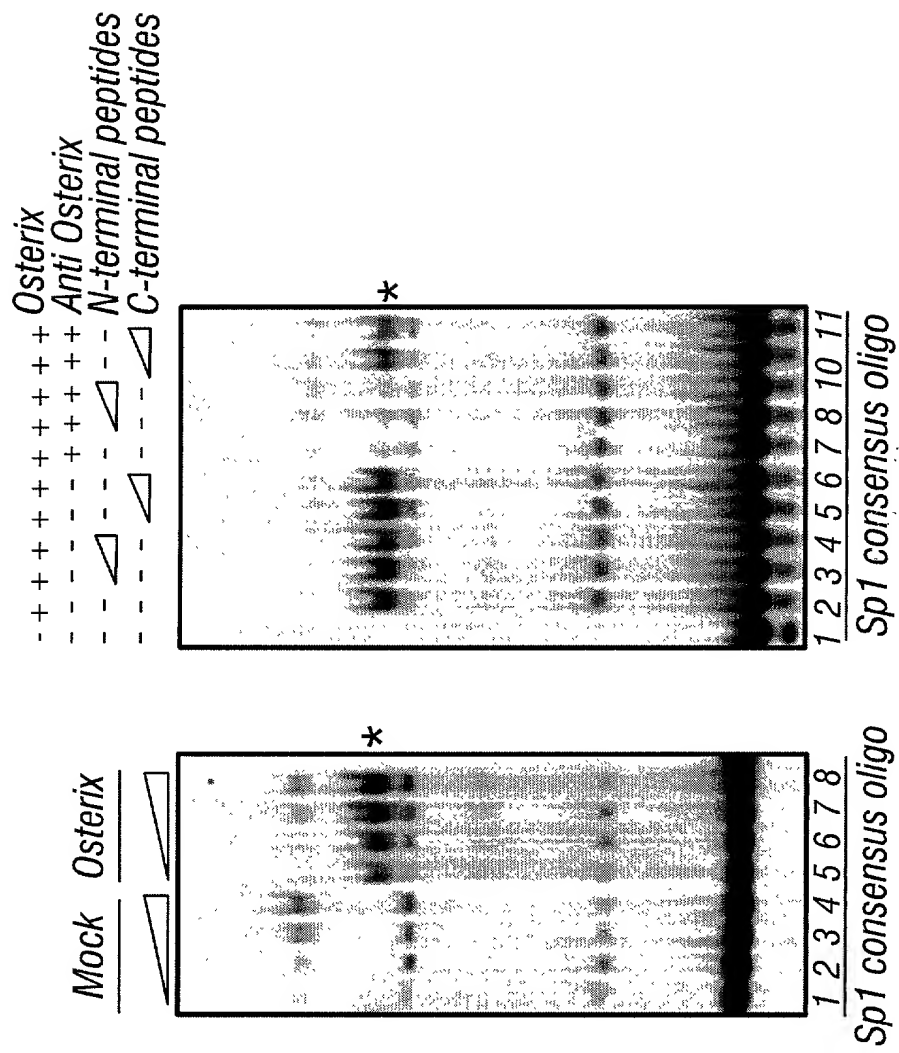
**FIG. 4A**



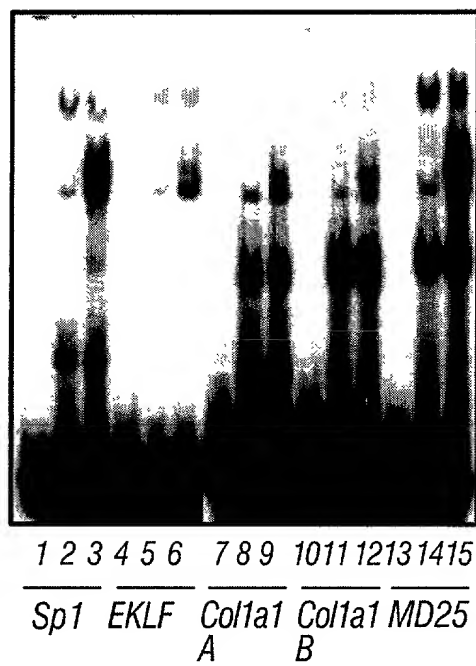
**FIG. 4B**



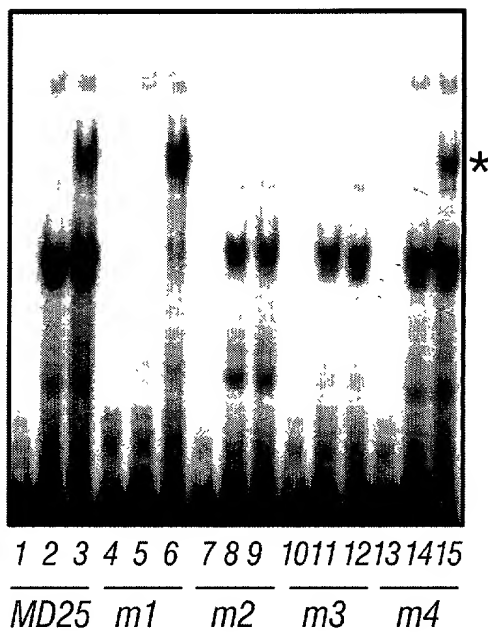
**FIG. 4C**

[illegible]

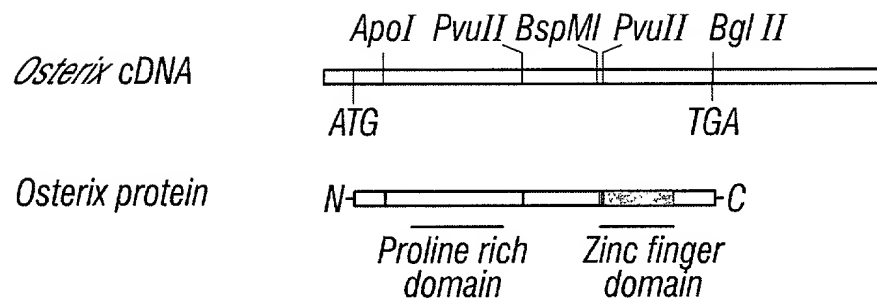




**FIG. 6A**



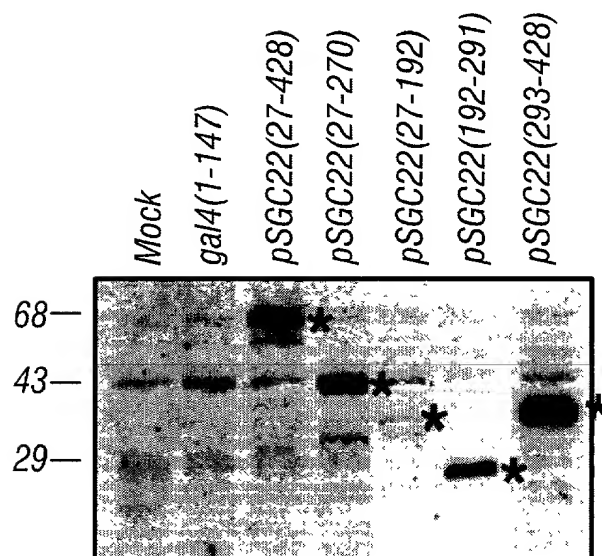
**FIG. 6B**



**FIG. 7A**

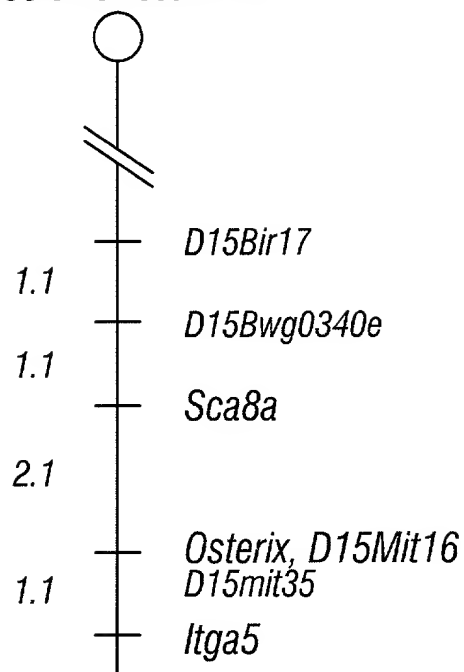
| <u>Constructs</u> | <u>Transcriptional activity</u> |
|-------------------|---------------------------------|
| gal4(1-147)       | 1.0                             |
| pSGC22(27-428)    | 3.0                             |
| pSGC22(27-270)    | 127.3                           |
| pSGC22(27-192)    | 68.4                            |
| pSGC22(192-291)   | 0.6                             |
| pSGC22(293-428)   | 0.5                             |

**FIG. 7B**

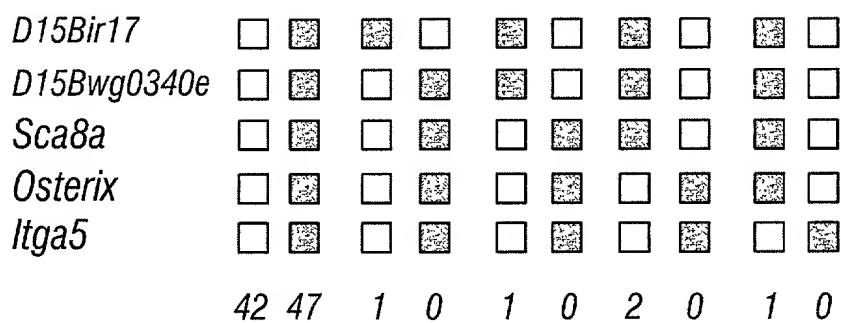


**FIG. 7C**

BSS Chromosome 15



**FIG. 8A**



**FIG. 8B**

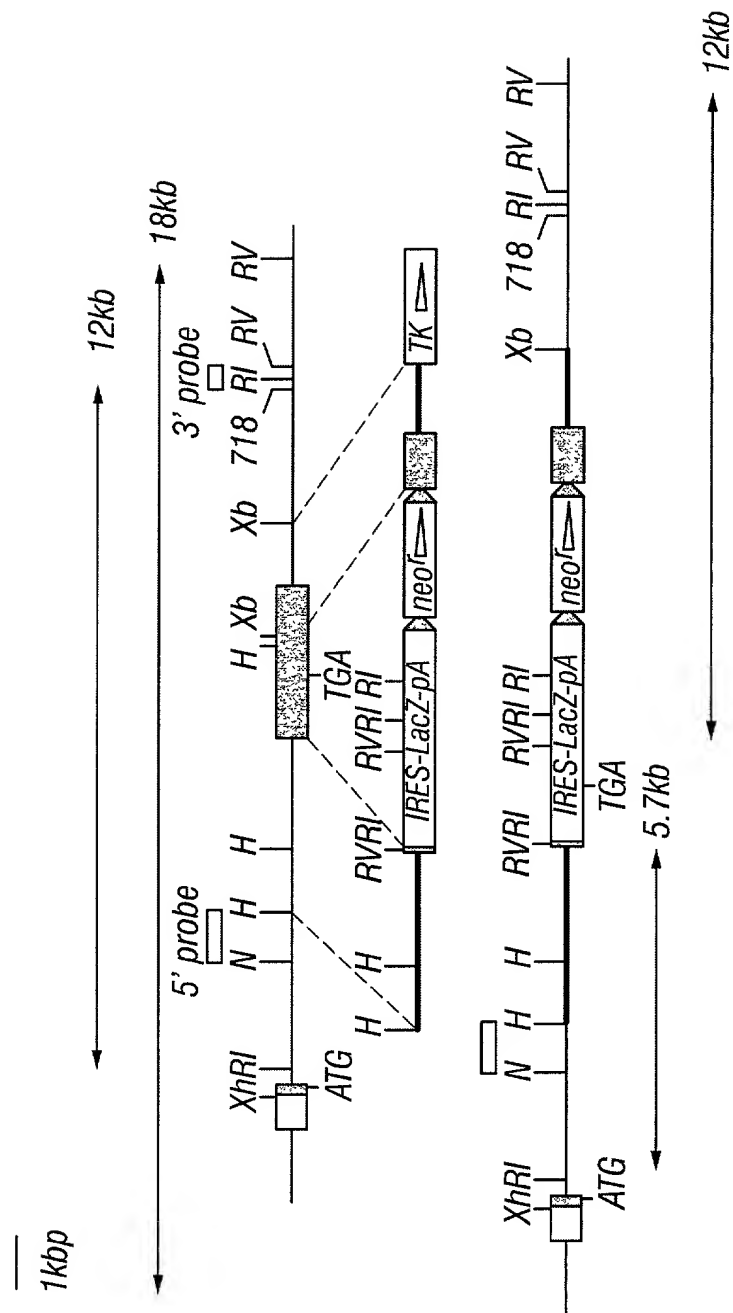
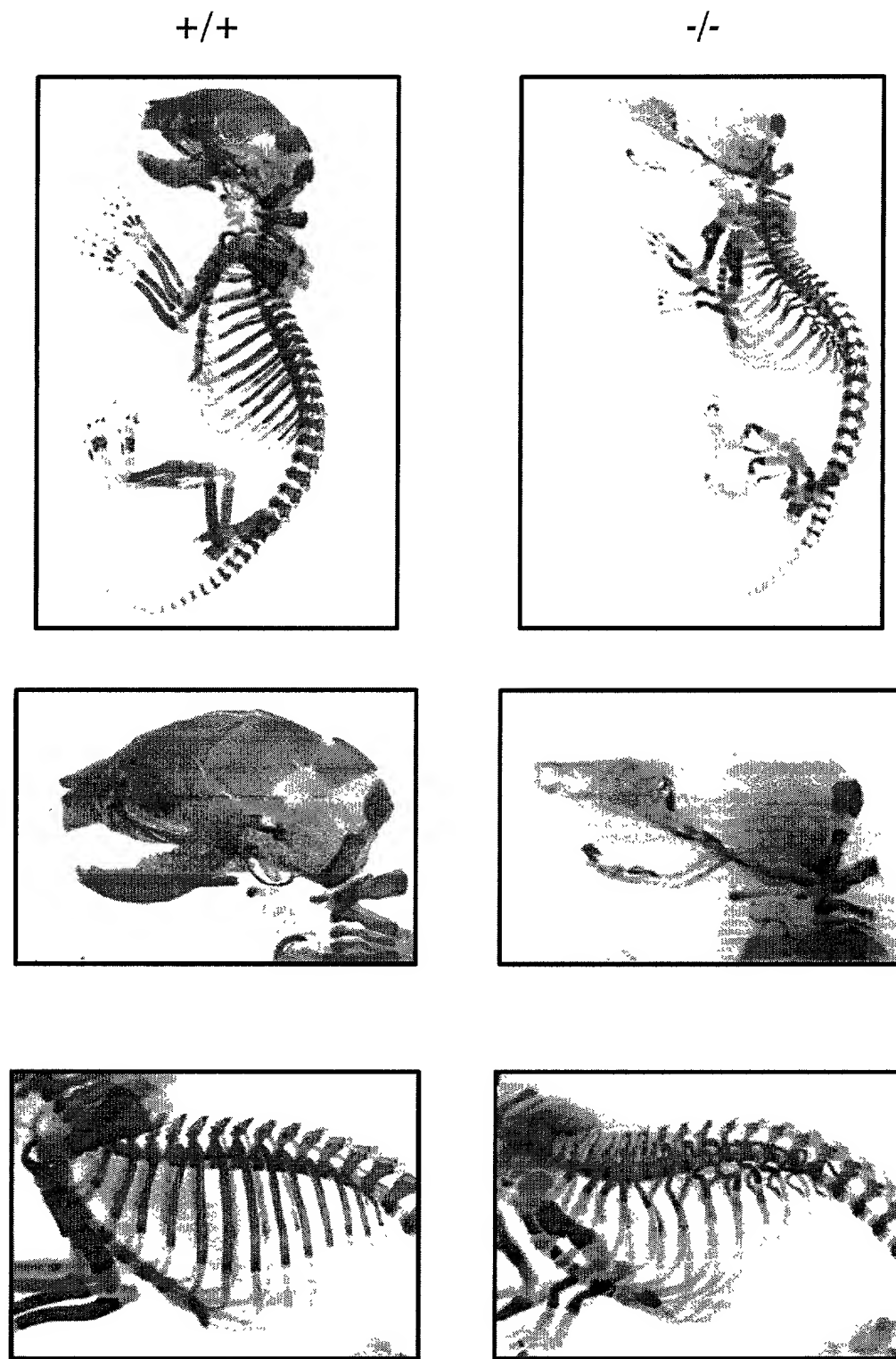


FIG. 8



**FIG. 9**

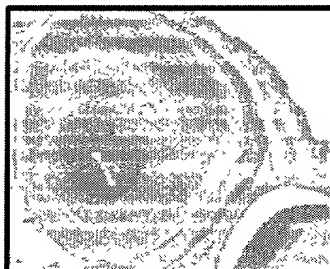
*Osterix +/+*

*Osterix -/-*

*AB/HT*



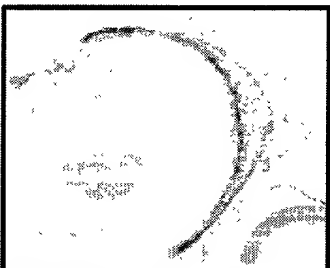
*Von Kossa*



*Collal*



*BSP*



*Cbfa1*



**FIG. 10A**

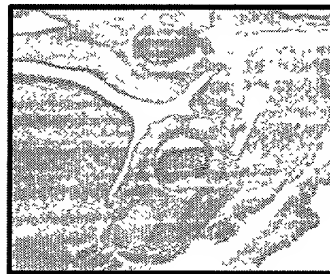
*Osterix +/+*

*Osterix -/-*

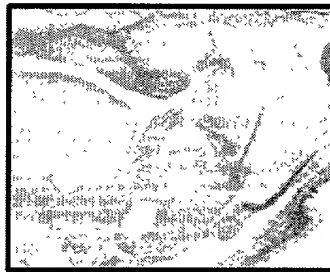
*AB/HT*



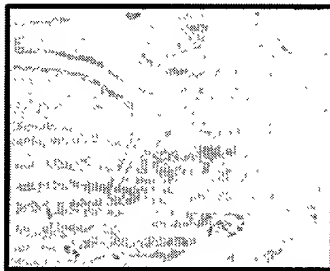
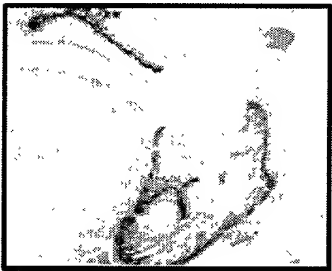
*Von Kossa*



*Collal*



*BSP*



*Cbfa1*



**FIG. 10B**

***Osterix* +/+**

***Osterix -/-***

**AB/HT**

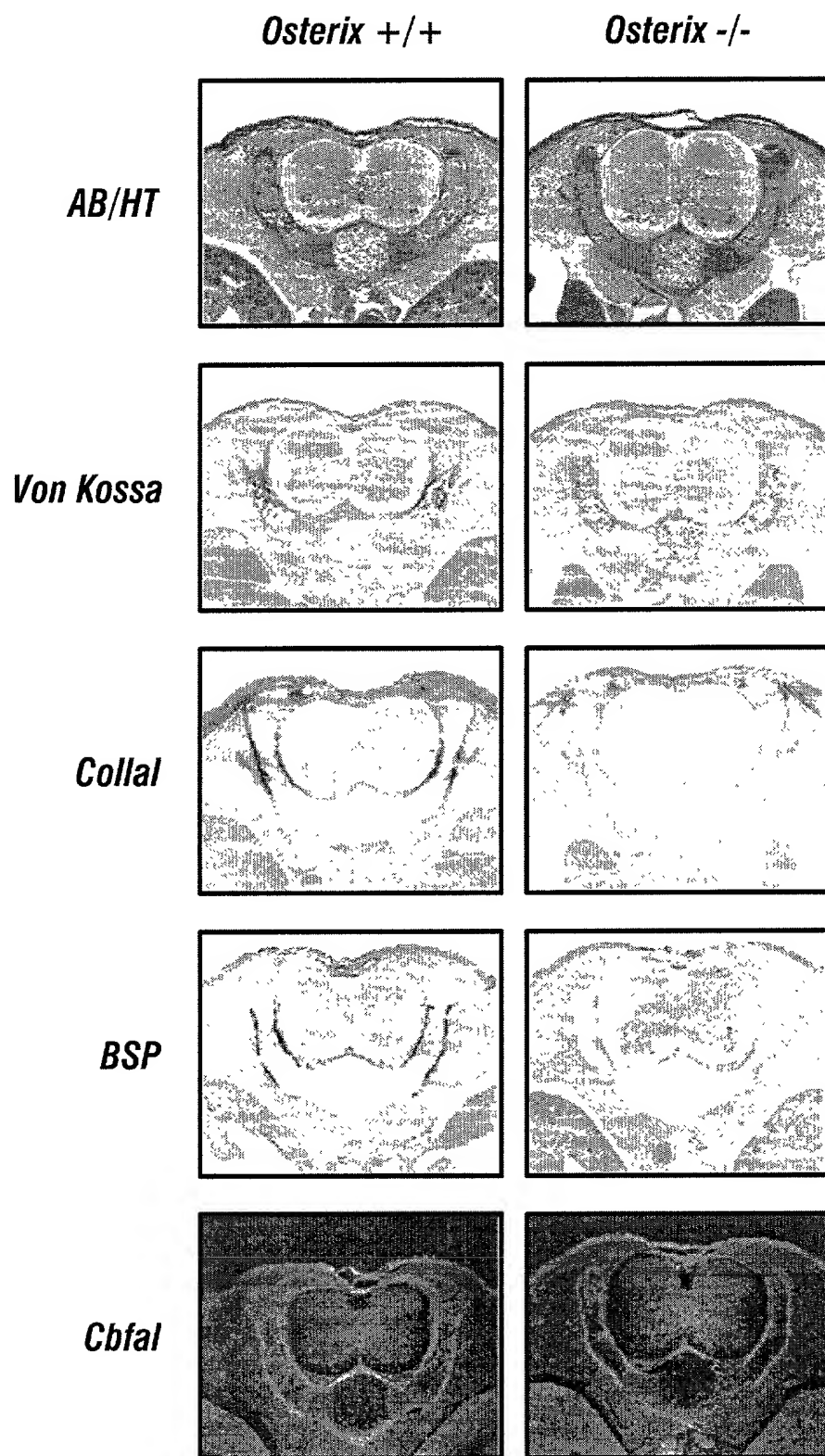
**Von Kossa****Collal**

**BSP**

***Cbfal***

**FIG. 10C**





**FIG. 10D**